

OIIPE

## RAW SEQUENCE LISTING

DATE: 12/13/2001

PATENT APPLICATION: US/09/908,943A

TIME: 13:45:04

Input Set : A:\00281A.txt

Output Set: N:\CRF3\12132001\I908943A.raw

ENTERED

4 <110> APPLICANT: Yan, Riqiang  
 5 Tomasselli, Alfredo G.  
 6 Gurney, Mark E.  
 7 Emmons, Thomas L.  
 8 Bienkowski, Mike J.  
 9 Heinrikson, Robert L.

11 <120> TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY  
 13 <130> FILE REFERENCE: 29915/00281A.US1  
 15 <140> CURRENT APPLICATION NUMBER: 09/908,943A  
 16 <141> CURRENT FILING DATE: 2001-07-19  
 18 <150> PRIOR APPLICATION NUMBER: 60/219,795  
 19 <151> PRIOR FILING DATE: 2000-07-19  
 21 <160> NUMBER OF SEQ ID NOS: 197  
 23 <170> SOFTWARE: PatentIn Ver. 2.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 2070  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
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 33 ctgaggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
 34 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240  
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 36 gtgggtgctg ccccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360  
 37 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
 38 ctgggcaccg acctggttaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480  
 39 gctgccatca ctgaatcaga caagtcttc atcaacggt ccaactggga aggcacctct 540  
 40 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600  
 41 ctggttaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660  
 42 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720  
 43 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780  
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 49 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
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 56 aagtgaggag gcccatgggc agaagataga gattccctct gaccacacct ccgtggttca 1560  
 57 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggacctcc 1620  
 58 ccaccacca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680

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61 ttgtccacca ttcttttaaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
62 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
63 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
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77 20 25 30
79 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
80 35 40 45
82 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
83 50 55 60
85 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
86 65 70 75 80
88 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
89 85 90 95
91 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
92 100 105 110
94 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
95 115 120 125
97 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
98 130 135 140
100 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
101 145 150 155 160
103 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
104 165 170 175
106 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
107 180 185 190
109 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
110 195 200 205
112 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
113 210 215 220
115 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
116 225 230 235 240
118 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
119 245 250 255
121 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
122 260 265 270
124 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
125 275 280 285
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Input Set : A:\00281A.txt

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133 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
134      325      330      335
136 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
137      340      345      350
139 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
140      355      360      365
142 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
143      370      375      380
145 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
146 385      390      395      400
148 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
149      405      410      415
151 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
152      420      425      430
154 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
155      435      440      445
157 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
158      450      455      460
160 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
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166 Ile Ser Leu Leu Lys
167      500
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178 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag ggcagcttt 180
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189 agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
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191 gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcattctca 960
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195 tttgatcggg ccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
196 ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
197 aacattccac agacagatga gtcaaccctc atgaccatag cctatgtcat ggctgccatc 1320
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199 ctgcgccagc agcatgatga ctttgtgat gacatctccc tgctgaagtg aggaggcca 1440
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202 ctctgccttg atggagaagg aaaaggctgg caagggtgggt tccagggact gtacctgtag 1620
203 gaaacagaaa agagaagaaa gaagcactct gctggcgga atactcttg tcacctcaa 1680
204 ttttaagtcg gaaattctgc tgcctgaaac ttcagccctg aacctttgtc caccattcct 1740
205 ttaaattctc caacccaaag tattcttctt ttcttagttt cagaagtact ggcatacac 1800
206 gcaggttacc ttggcgtgtg tccctgtggt accctggcag agaagagacc aagcttggtt 1860
207 ccctgctggc caaagtcagt aggagaggat gcacagtttg ctatttgctt tagagacagg 1920
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222 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
223 35 40 45
225 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
226 50 55 60
228 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
229 65 70 75 80
231 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
232 85 90 95
234 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
235 100 105 110
237 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
238 115 120 125
240 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
241 130 135 140
243 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
244 145 150 155 160
246 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
247 165 170 175
249 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
250 180 185 190
252 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
253 195 200 205
255 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
256 210 215 220

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258 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
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261 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
262                245                250                255
264 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
265                260                265                270
267 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
268                275                280                285
270 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
271                290                295                300
273 Cys Trp Gln Ala Gly Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
274 305                310                315                320
276 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
277                325                330                335
280 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
281                340                345                350
283 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
284                355                360                365
286 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
287                370                375                380
289 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
290 385                390                395                400
292 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
293                405                410                415
295 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
296                420                425                430
298 Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
299                435                440                445
301 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
302                450                455                460
304 His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
305 465                470                475
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313 <220> FEATURE:
314 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
315 peptide sequence
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/908,943A

DATE: 12/13/2001

TIME: 13:45:06

Input Set : A:\00281A.txt

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**VERIFICATION SUMMARY**

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Input Set : A:\00281A.txt

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